

CACGCGTCCGCCCACGCGTCCGGTGAGACAGAGGCAAAACAAAGGTGCTGAAAGCCAGAC
1 -----+-----+-----+-----+-----+-----+ 60
GTGCGCAGGCGGGTGCGCAGGCCACTCTGTCTCCGTTTTGTTCCACGACTTTTCGGTCTG
a H A S A H A S G E T E A K Q R C * K P D -
ATGGAGTCAGAGATGAGTGATCCTCAGCCATTGCAGGAGGAAAGATATGATATGTCAGGT
61 -----+-----+-----+-----+-----+-----+ 120
TACCTCAGTCTCTACTCACTAGGAGTCGGTAACGTCCTCTTCTATACTATACAGTCCA
a M E S E M S D P Q P L Q E E R Y D M S G -
GCCCCGCTGGCCCTGACGCTGTGTGTACCAAAGCCCGGGAGGGTCCGAGGTAgACATG
121 -----+-----+-----+-----+-----+-----+ 180
CGGGCGGACCGGGACTGCGACACACAGTGGTTTCGGGCCCTCCCAAGGCTCCATCTGTAC
a A R L A L T L C V T K A R E G S E V D M -
GAGGCCCTGGAACGCATGTTCCGTTACCTGAAATTTGAAAGCACCATGAAGAGGGATCCC
181 -----+-----+-----+-----+-----+-----+ 240
CTCCGGGACCTTGCGTACAAGGAATGGACTTTAACTTTCGTGGTACTTCTCCCTAGGG
a E A L E R M F R Y L K F E S T M K R D P -
ACGCCCAGCAATTTCTGGAAGAGTTGGATGAATTTGAGCAGACCATAGATAATTGGGAA
241 -----+-----+-----+-----+-----+-----+ 300
TGCGGGTCGTTAAAGACCTTCTCAACCTACTTAAAGTCGTCTGGTATCTATTAACCTT
a T A Q Q F L E E L D E F Q Q T I D N W E -
GAGCCTGTCAGCTGTGCCTTTGTGGTACTCATGGCACATGGTGAGGAAGGCCTCCTCAAG
301 -----+-----+-----+-----+-----+-----+ 360
CTCGGACAGTCGACACGGAAACACCATGAGTACCGTGTACCACTCCTTCCGGAGGAGTTC
a E P V S C A F V V L M A H G E E G L L K -
GGAGAAGATGAGAAGATGGTCAGACTAGAAGACCTTTTTGAAGTCTTGAACAACAAGAAC
361 -----+-----+-----+-----+-----+-----+ 420
CCTCTTCTACTCTTCTACCAGTCTGATCTTCTGGAAAACTTCAGAACTTGTTGTTCTTG
a G E D E K M V R L E D L F E V L N N K N -
TGCAAGGCCCTGAGAGGCAAGCCAAAGGTGTACATCATCCAGGCTTGTAGAGGAGAGCAC
421 -----+-----+-----+-----+-----+-----+ 480
ACGTTCCGGGACTCTCCGTTCCGTTTCCACATGTAGTAGGTCCGAACATCTCCTCTCGTG

Fig. 1A

```

a   C K A L R G K P K V Y I I Q A C R G E H   -
    AGAGACCCCGGTGAGGAACTACGTGGAATGAGGAACTAGGTGGAGATGAGGAACTNGGT
481 -----+-----+-----+-----+-----+-----+ 540
    TCTCTGGGGCCACTCCTTGATGCACCTTTACTCCTTGATCCACCTCTACTCCTTGANCCA

a   R D P G E E L R G N E E L G G D E E L G   -
    GGAGATGAGGTTGCTGTGCTCAAGAACAACCCCAAAGTATCCCAACCTATACGGATACC
541 -----+-----+-----+-----+-----+-----+ 600
    CCTCTACTCCAACGACACGAGTTCTTGTTGGGGTTTCATAGGGTTGGATATGCCTATGG

a   G D E V A V L K N N P Q S I P T Y T D T   -
    CTCCACATCTACTCCACGGTAGAGGGGTACCTCTCCTATAGACATGACGAGAAAGGCTCT
601 -----+-----+-----+-----+-----+-----+ 660
    GAGGTGTAGATGAGGTGCCATCTCCCATGGAGAGGATATCTGTACTGCTCTTTCCGAGA

a   L H I Y S T V E G Y L S Y R H D E K G S   -
    GGCTTCATCCAGACCCTGACGGATGTGTTTCATTCATAAAAAAGGATCCATCTTAGAACTG
661 -----+-----+-----+-----+-----+-----+ 720
    CCGAAGTAGGTCTGGGACTGCCTACACAAGTAAGTATTTTTCTAGGTAGAATCTTGAC

a   G F I Q T L T D V F I H K K G S I L E L   -
    ACAGAAGAGATCACCCGACTTATGGCAAACACGGAGGTGATGCAGGAAGGAAAACCAAGG
721 -----+-----+-----+-----+-----+-----+ 780
    TGTCTTCTCTAGTGGGCTGAATACCGTTTGTGCCTCCACTACGTCCTTCCTTTTGGTTCC

a   T E E I T R L M A N T E V M Q E G K P R   -
    AAAGTGAACCCTGAAGTCCAAAGCACCCCTCCGGAAGAAGCTCTATTTGCAATAAAAGAGA
781 -----+-----+-----+-----+-----+-----+ 840
    TTTCAC TTGGGACTTCAGGTTTCGTGGGAGGCCTTCTTCGAGATAAACGTTATTTCTCT

a   K V N P E V Q S T L R K K L Y L Q * K R   -
    GGGCAGGGAT
841 -----+ 850
    CCCGTCCCTA

a   G Q G   -
    
```

Fig. 1B

casp-11 -----
 casp-12 -----MAARRTHERDPIYKIKGLAKMLDGV 26
 casp-1 -----MADKILRAKRQFINSVSGTINGL 25
 casp-3 -----
 casp-7 -----
 casp-6 -----
 casp-8 MDFQSCDAIAEELGSEDLAALKFLCLDYIPHKLETIEDAQLFLRLREKGMLEEGNLSFLKELLFHISRWDLLVNFDCNREEMVRELDRPQCPRFL 100
 casp-2 -----MAAPSGRSQSSLHRKGLMAADRRSRI LAVCGMHPDHQETLKKNRVVLAKQLL 52
 casp-14 -----

 casp-11 -----MAENKHPDKPLKVLQGLKEVL . TEYLEKLVSQNVKLKEEDKQKFNNARSOKRWV . DAMKKKHSKVGEMLLQTFFSVDPG 82
 casp-12 FDDLVEKNVLNGDELLKIGESASFILNKAENLVENFLEKTDMAKIFAGHTANSQEQLS LQFSNDEDDGPQKICTPSSPSESERKVEDDEMEVNAGLAHE 126
 casp-1 LDELLEKRVLNQEEMDKIKLANITAMDKARDLCDHVSKKGPOASQIFITYICNEDCYLAGILELQSAPSAETFVATEDSKGGHPSSSETKEEQN . KEDG 123
 casp-3 -----MENNKTSV 8
 casp-7 -----MTDDQCAAELEKVDSSSEDGVDAPDRSSI 31
 casp-6 -----
 casp-8 PYRSCSFRLEEVELELRSFKLLNNEIPCKLEDDLILLEIFVEMEKRTMLAENNELTSLKICDQVNSLLGKIEDYERSSTERRMSLEGREELPPSV 200
 casp-2 LSELLEHLLKEDIITLEMRELIAKGGSFQNVLLNLLPKRGPQAFDAFCEALRETRQGHLEDLLLTTLSDIQHVLPLPCDYDTSLPFSVCESCPPHK 152
 casp-14 -----

 casp-11 SHHGEANLEMEPEESLNTLKLCSPEEFTRLCREKTQEIYPIKEAN . GRTRKALICNTEFKHLSLRYGANFDIIGMKGLLEDLGYDVVVKELTAEGME 181
 casp-12 SHMLTAPHGLQSSEVDTLKLCPRDQFCIKTERAKEIYPVMEKE . GRTRLALICNKKFDYLFDRDNADTDILNMQELLENLGYSVLKENLTAQEME 225
 casp-1 TFPGLTG TLKFCPLEKAQKLWKENPSEIYPIMNTT . TRTRLALICNTEFQHLSPRVGAQVDLREMKLLLEDLGYTVKVENLTAEMV 211
 casp-3 DSKSINNFEVKTIHGSKSVDSGIYLDSSYKMDYPEMGICIIINNKNFHS TGMSSRSRGTDVDAANLRETFMGLKYCVRNKNDLTREDIL 97
 casp-7 ISSILLKKRNASAGPVRTGRDVPPTYLYRMDYQKMGKCIINNKNFKA TGMVVRNGTDKDAGALFKCFQNLGFVTVHNDSCAKMQ 120
 casp-6 -----MTETDGFYKSREVFDAEQYKMDHKRRGVALIFNHERFFWH LTLPERRGTNADRDNLTRRFSDLGFEVKCFNDLRAEELL 80
 casp-8 LDEMSLKMAELCDSPREQDSERTSDKVYQMNKPRGYCLINNHDFSKA REDITQLRKMCKRGTDCKEALSKTFKELHFEIVSYDDCTANEIH 296
 casp-2 QLRLSTDATEHSLDNGDGPCLLVKPCPEFYQAHYQLAYRLQSQPRGLALVLSNVHFTGEKDLFRSGGDVDHTLVTFLKLLGYNVHVLHDQTAQEMQ 252
 casp-14 -----MESEMSDPQLQEERYDMSGARLALTL CVTK AREGSEVDMEALERMFRYLKFESTMKRDPTAQQL 66

 casp-11 SEMDKFAAL SEHQTSDSSTFLVMSHGTLHGICGTMHSEKTPDVLQYDTIYQIFNCHCPGLRDKPKVII IQACRGNGSGEMWIRESSKPQLCRGVDLP 279
 casp-12 TELMQFAGR PEHQSSDSSTFLVMSHGILEGICGVKHRNKKPDVLDHDTIFKIFNNSNCRSLRNKPKIL IQACRGNGYNGTIWV . STNKGIATADTDEE 322
 casp-1 KEVKEFAAC PEHKTSDSTFLVMSHGIEGICGTTYSNEVSILKVDITFQMMNTLKCPSLKDKPKVII IQACRGEKQGVVLLKDS VRDSEED 304
 casp-3 ELMDSVSK EDHSKRSSFVCVILSHGDEGVIYGTNGP VELKLTSTFRGDYCRSLTGKPKLFI IQACRGTELDGCI ETDG G 177
 casp-7 DLLRKASE EDHSNSACFACVLLSHGEEDLYGKGDV TPIKDLTAHFRGDRCKTLLEKPKLFI IQACRGTELDGI QADS G 200
 casp-6 LKTHEVST SSHIDADCFCVFLSHGEGNHVYAYDAK TEIQTLTGLFKGDKCQSLVGKPKIFI IQACRGSHQDVVPVPLDMVDHQTOK LD 169
 casp-8 EILEGYQS ADHNKDCFCILSHGDKGVVYGTGK EASYDLTSYFTGSKCPSLSGKPKIFI IQACRGSNFQKGVPEAGFEQQNHT LE 356
 casp-2 EKLQNFQA . LPAHRVTD SVC . VALLSHGVEGGIYGVGDK LLQLQEVFRLFDNANCPSLQNKPKMFI IQACRGDETRGVDDQDGKNHTQSPGCEE 345
 casp-14 EELDEFQQTIDNWEPEVSCAFVLLMAHGEEGLLKGDEK MVRLEDLFEVLNNKNCKALRGKPKVYI IQACRGEHRDPGEELRGNEELGGDEELGG 161

Fig. 2A-1

```

casp-11 RNMEA...DAVKLSHVEKDFIAFYSTTPHHSYRDKTGGSYFITRLISCFRKHACSCHLFDIFLKVQSFEEKASIHSMPTIDRATLTRFYLFPGN-- 373
casp-12 RVLSCKW.NNSITKAHVETDFIAFKSSTPHNISWRVKTGSLFISKLIDCFKKYCWCYHLEEIFRKVQHSFEVPGELTQMPTIERVSMTRYFYLFPGN-- 419
casp-1  FLTDAIFEDDGIKKAHIEKDFIAFCSTPDNVSWRHPVRGSLFIESLIKHMKEYAWSCDLEDIFRKVRFSFEQPEFRLQMPTADRVTLTKRFYLFPGH-- 402
casp-3  ..TDEEMAC...QKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCSMLKLY..AHKLEFMHILTRVNRKVATEFESFSLDSTFHAKKQIPCIVSMLT 270
casp-7  ..PINDIDANPRNKIPVEADFLFAYSTVPGYYSWRNPGKGSWFVQALCSILNEH..GKDLEIMQILTRVNDRVARHFESQSDDPREFNEKKQIPCMVSMLT 296
casp-6  ..NVTQVDAASVYTLFAGADFLMCYSVAEGYYSHRETVNGSWYIQDLCEMLARY..GSSLEFTELLTLVNRKVSQRRVDFCKDPAIGKKQVPCFASMLT 265
casp-8  ..VDS...SSHKNYIPDEADFLGMATVLMCVSYRDPVNGTWYIQSLCQSLRERC.PQGGDILSILTGVDVSN.....KDDRRNKGKQMPQPTFTLR 474
casp-2  ..SDAGKEELMKMRLPTRSDMICGYACLKGNAAMRNTKRGSWYIEALTQVFSERA.C.DMHVADMLVKVNALIKER.EGYAPGTEFHRCKEMSEYCYSTLC 440
casp-14 ..DEVAVLKNNPQSIPTYTDTLHIYSTVEGYLSYRDEKGGSGFIQTLTDVFIHKK.G.S..ILELTEITRLMANT.EVMQEGKP...RKVNPEVQSTLR 251
    
```

```

casp-11 -----
casp-12 -----
casp-1  -----
casp-3  KELYFYH----- 277
casp-7  KELYFSR----- 303
casp-6  KKLHFCPKPSK- 276
casp-8  KKL----- 477
casp-2  QQLYLFPGYPPT 452
casp-14 KKLYLQ----- 257
    
```

Fig. 2A-2

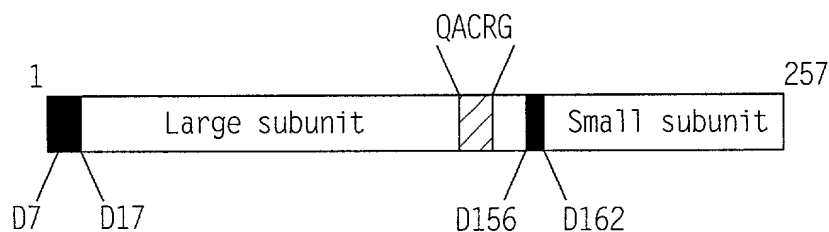


Fig. 2B

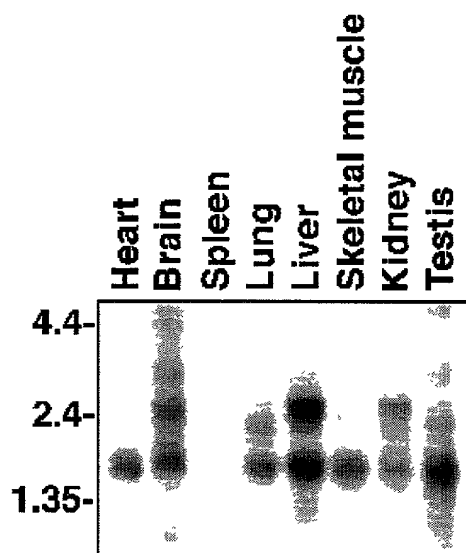


Fig. 3

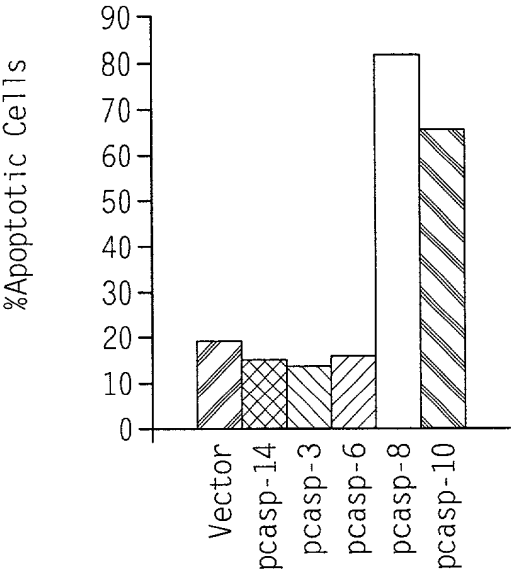


Fig. 4

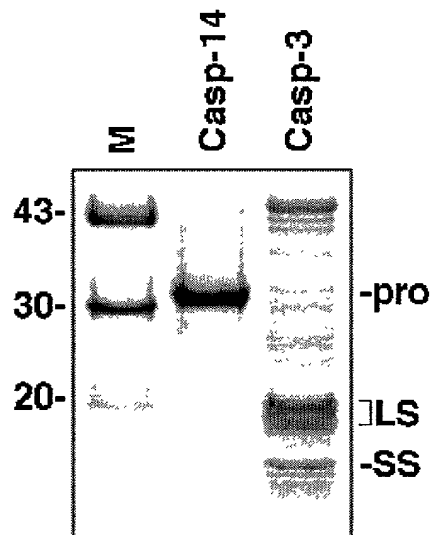


Fig. 5A

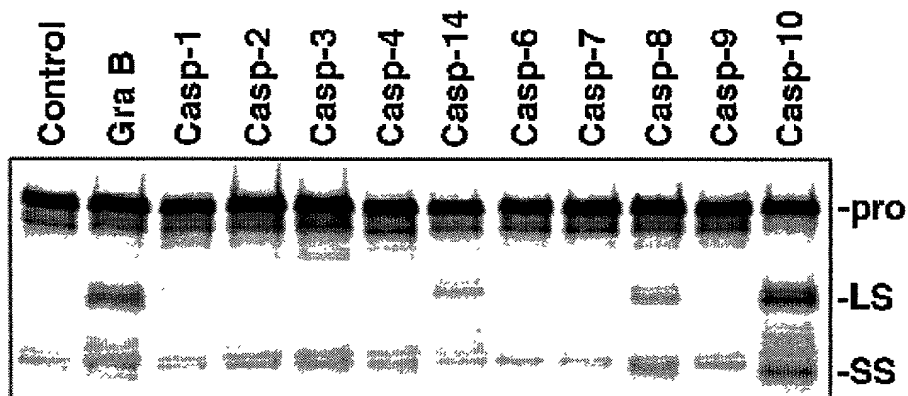


Fig. 5B

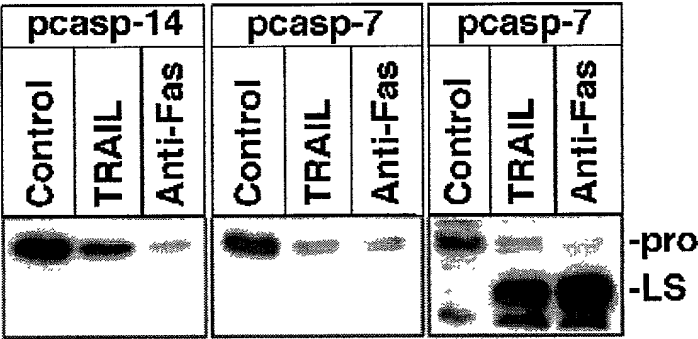


Fig. 5C

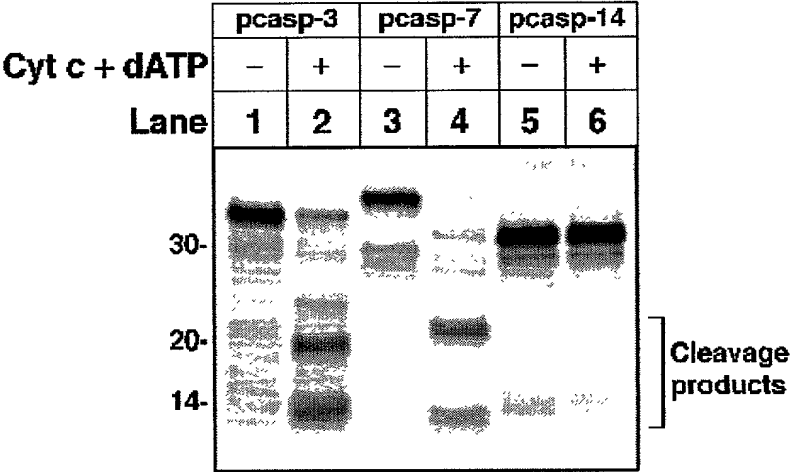


Fig. 6


```

aggatcagac aaggggtgctg agagccggga ctcacaacca aaggagaa atg agc aat 57
                                         Met Ser Asn
                                         1

ccg cggtct ttg gaa gag gag aaa tat gat atg tca ggt gcc cgc ctg 105
Pro Arg Ser Leu Glu Glu Glu Lys Tyr Asp Met Ser Gly Ala Arg Leu
      5              10              15

gcc cta ata ctg tgt gtc acc aaa gcc cgg gaa ggt tcc gaa gaa gac 153
Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu Gly Ser Glu Glu Asp
      20              25              30              35

ctg gat gct ctg gaa cac atg ttt cgg cag ctg aga ttc gaa agc acc 201
Leu Asp Ala Leu Glu His Met Phe Arg Gln Leu Arg Phe Glu Ser Thr
              40              45              50

atg aaa aga gac ccc act gcc gag caa ttc cag gaa gag ctg gaa aaa 249
Met Lys Arg Asp Pro Thr Ala Glu Gln Phe Gln Glu Glu Leu Glu Lys
              55              60              65

ttc cag cag gcc atc gat tcc cgg gaa gat ccc gtc agt tgt gcc ttc 297
Phe Gln Gln Ala Ile Asp Ser Arg Glu Asp Pro Val Ser Cys Ala Phe
              70              75              80

gtg gta ctc atg gct cac ggg agg gaa ggc ttc ctc aag gga gaa gat 345
Val Val Leu Met Ala His Gly Arg Glu Gly Phe Leu Lys Gly Glu Asp
      85              90              95

ggg gag atg gtc aag ctg gag aat ctc ttc gag gcc ctg aac aac aag 393
Gly Glu Met Val Lys Leu Glu Asn Leu Phe Glu Ala Leu Asn Asn Lys
100              105              110              115

aac tgc cag gcc ctg cga gct aag ccc aag gtg tac atc ata cag gcc 441
Asn Cys Gln Ala Leu Arg Ala Lys Pro Lys Val Tyr Ile Ile Gln Ala
              120              125              130

tgt cga gga gaa caa agg gac ccc ggt gaa aca gta ggt gga gat gag 489
Cys Arg Gly Glu Gln Arg Asp Pro Gly Glu Thr Val Gly Gly Asp Glu
              135              140              145

att gtg atg gtc atc aaa gac agc cca caa acc atc cca aca tac aca 537
Ile Val Met Val Ile Lys Asp Ser Pro Gln Thr Ile Pro Thr Tyr Thr
              150              155              160
    
```

Fig. 7A

```

gat gcc ttg cac gtt tat tcc acg gta gag gga tac atc gcc tac cga 585
Asp Ala Leu His Val Tyr Ser Thr Val Glu Gly Tyr Ile Ala Tyr Arg
    165                170                175

cat gat cag aaa ggc tca tgc ttt atc cag acc ctg gtg gat gtg ttc 633
His Asp Gln Lys Gly Ser Cys Phe Ile Gln Thr Leu Val Asp Val Phe
    180                185                190                195

acg aag agg aaa gga cat atc ttg gaa ctt ctg aca gag gtg acc cgg 681
Thr Lys Arg Lys Gly His Ile Leu Glu Leu Leu Thr Glu Val Thr Arg
                200                205                210

cgg atg gca gaa gca gag ctg gtt caa gaa gga aaa gca agg aaa acg 729
Arg Met Ala Glu Ala Glu Leu Val Gln Glu Gly Lys Ala Arg Lys Thr
                215                220                225

aac cct gaa atc caa agc acc ctc cgg aaa cgg ctg tat ctg cag tag 777
Asn Pro Glu Ile Gln Ser Thr Leu Arg Lys Arg Leu Tyr Leu Gln
    230                235                240
    
```

Fig. 7B

```

aggatcagac aagggtgctg agagccgga ctcacaacca aaggagaa atg agc aat 57
                                         Met Ser Asn
                                         1

ccg cgg tct ttg gaa gag gag aaa tat gat atg tca ggt gcc cgc ctg 105
Pro Arg Ser Leu Glu Glu Glu Lys Tyr Asp Met Ser Gly Ala Arg Leu
      5              10              15

gcc cta ata ctg tgt gtc acc aaa gcc cgg gaa ggt tcc gaa gaa gac 153
Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu Gly Ser Glu Glu Asp
      20              25              30              35

ctg gat gct ctg gaa cac atg ttt cgg cag ctg aga ttc gaa agc acc 201
Leu Asp Ala Leu Glu His Met Phe Arg Gln Leu Arg Phe Glu Ser Thr
              40              45              50

atg aaa aga gac ccc act gcc gag caa ttc cag gaa gag ctg gaa aaa 249
Met Lys Arg Asp Pro Thr Ala Glu Gln Phe Gln Glu Glu Leu Glu Lys
              55              60              65

ttc cag cag gcc atc gat tcc cgg gaa gat ccc gtc agt tgt gcc ttc 297
Phe Gln Gln Ala Ile Asp Ser Arg Glu Asp Pro Val Ser Cys Ala Phe
              70              75              80

gtg gta ctc atg gct cac ggg agg gaa ggc ttc ctc aag gga gaa gat 345
Val Val Leu Met Ala His Gly Arg Glu Gly Phe Leu Lys Gly Glu Asp
      85              90              95

ggg gag atg gtc aag ctg gag aat ctc ttc gag gcc ctg aac aac aag 393
Gly Glu Met Val Lys Leu Glu Asn Leu Phe Glu Ala Leu Asn Asn Lys
100              105              110              115

aac tgc cag gcc ctg cga gct aag ccc aag gtg tac atc ata cag gcc 441
Asn Cys Gln Ala Leu Arg Ala Lys Pro Lys Val Tyr Ile Ile Gln Ala
              120              125              130

tgt cga gga gaa caa agg gac ccc ggt gaa aca gta ggt gga gat gag 489
Cys Arg Gly Glu Gln Arg Asp Pro Gly Glu Thr Val Gly Gly Asp Glu
              135              140              145

att gtg atg gtc atc aaa gac agc cca caa acc atc cca aca tac aca 537
Ile Val Met Val Ile Lys Asp Ser Pro Gln Thr Ile Pro Thr Tyr Thr
      150              155              160
    
```

Fig. 8A

gat gcc ttg cac gtt tat tcc acg gta gag gga ccc acg ccc ttc cag 585
 Asp Ala Leu His Val Tyr Ser Thr Val Glu Gly Pro Thr Pro Phe Gln
 165 170 175

gat ccc ctc tac cta ccc tct gaa gct ccc ccg aac cca cct ctc tgg 633
 Asp Pro Leu Tyr Leu Pro Ser Glu Ala Pro Pro Asn Pro Pro Leu Trp
 180 185 190 195

aat tcc cag gat aca tcg cct acc gac atg atc aga aag gct cat gct 681
 Asn Ser Gln Asp Thr Ser Pro Thr Asp Met Ile Arg Lys Ala His Ala
 200 205 210

tta tcc aga ccc tgg tgg atg tgt tca cga aga gga aag gac ata tct 729
 Leu Ser Arg Pro Trp Trp Met Cys Ser Arg Arg Gly Lys Asp Ile Ser
 215 220 225

tgg aac ttc tgacagaggt gacccggcgg atggcagaag cagagctggt 778
 Trp Asn Phe
 230

tcaagaagga aaagcaagga aaacgaaccc tgaaatccaa agcaccctcc ggaaacggct 838

gtatctgcag tag 851

Fig. 8B

```

aggatcagac aaggggtgctg agagccggga ctcacaacca aaggagaa atg agc aat 57
                                         Met Ser Asn
                                         1

ccg cgg tct ttg gaa gag gag aaa tat gat atg tca ggt gcc cgc ctg 105
Pro Arg Ser Leu Glu Glu Glu Lys Tyr Asp Met Ser Gly Ala Arg Leu
      5              10              15

gcc cta ata ctg tgt gtc acc aaa gcc cgg gaa ggt tcc gaa gaa gaa 153
Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu Gly Ser Glu Glu Glu
      20              25              30              35

gag ctg gaa aaa ttc cag cag gcc atc gat tcc cgg gaa gat ccc gtc 201
Glu Leu Glu Lys Phe Gln Gln Ala Ile Asp Ser Arg Glu Asp Pro Val
              40              45              50

agt tgt gcc ttc gtg gta ctc atg gct cac ggg agg gaa ggc ttc ctc 249
Ser Cys Ala Phe Val Val Leu Met Ala His Gly Arg Glu Gly Phe Leu
              55              60              65

aag gga gaa gat ggg gag atg gtc aag ctg gag aat ctc ttc gag gcc 297
Lys Gly Glu Asp Gly Glu Met Val Lys Leu Glu Asn Leu Phe Glu Ala
              70              75              80

ctg aac aac aag aac tgc cag gcc ctg cga gct aag ccc aag gtg tac 345
Leu Asn Asn Lys Asn Cys Gln Ala Leu Arg Ala Lys Pro Lys Val Tyr
              85              90              95

atc ata cag gcc tgt cga gga gaa caa agg gac ccc ggt gaa aca gta 393
Ile Ile Gln Ala Cys Arg Gly Glu Gln Arg Asp Pro Gly Glu Thr Val
      100              105              110              115

ggt gga gat gag att gtg atg gtc atc aaa gac agc cca caa acc atc 441
Gly Gly Asp Glu Ile Val Met Val Ile Lys Asp Ser Pro Gln Thr Ile
              120              125              130

cca aca tac aca gat gcc ttg cac gtt tat tcc acg gta gag gga tac 489
Pro Thr Tyr Thr Asp Ala Leu His Val Tyr Ser Thr Val Glu Gly Tyr
              135              140              145

atc gcc tac cga cat gat cag aaa ggc tca tgc ttt atc cag acc ctg 537
Ile Ala Tyr Arg His Asp Gln Lys Gly Ser Cys Phe Ile Gln Thr Leu
      150              155              160
    
```

Fig. 9A

gtg gat gtg ttc acg aag agg aaa gga cat atc ttg gaa ctt ctg aca 585
Val Asp Val Phe Thr Lys Arg Lys Gly His Ile Leu Glu Leu Leu Thr
165 170 175

gag gtg acc cgg cgg atg gca gaa gca gag ctg gtt caa gaa gga aaa 633
Glu Val Thr Arg Arg Met Ala Glu Ala Glu Leu Val Gln Glu Gly Lys
180 185 190 195

gca agg aaa acg aac cct gaa atc caa agc acc ctc cgg aaa cgg ctg 681
Ala Arg Lys Thr Asn Pro Glu Ile Gln Ser Thr Leu Arg Lys Arg Leu
200 205 210

tat ctg cag tag 693
Tyr Leu Gln

Fig. 9B

```

1 MESEMSDPQPLQEERYDMGRLALTLCTKAREGSEVDMEALERMFRYL 50
  |||. |::|:||||||| ||||| ||::||| |||
1 ....MSNPRSLEEEKYDMGRLALTLCTKAREGSEEDLDALEHMFRL 46

51 KFESTMKRDPTAQFLEELDEFQQTIDNWEPPVSCAFVVLMAHGEEGLK 100
  :|||||||:| |||:| ||| |::|:||||||| |||
47 RFESTMKRDPTAEQFQEELEKFAQIDSREDPVSCAFVVLMAHGREGFLK 96

101 GEDEKMRLEDLFEVLNNKNCKALRGKPKVYIIQACRGEHRDPGEELRGN 150
  ||| |::|:| ||| |::|:| ||||| ||||| ||||
97 GEDGEMVKLENLFEALNNKNQALRAKPKVYIIQACRGEQRDPG..... 140

151 EELGGDEELGGDEVAVLKNPQSIPTYTDLHIYSTVEGYLSYRHDEKGS 200
  |.|||| |::|:| ||||| ||:|||||:|:|:|
141 ETVGGDE....IVMVIKDSPTIPTYDALHVYSTVEGYIAYRHDQKGS 185

201 GFIQTLTDVFIHKKSILELTEITRLMANTEVMQEGKPRKVNPEVQSTL 250
  ||||| ||| :|| |||| |::| || |..|||| |||:||||
186 CFIQTLVDVFTKRKGHILELLTEVTRMAEELVQEGKARKTNPEIQSTL 235

251 RKKLYLQ* 257
  ||:||||
236 RKRLYLQ* 242
  
```

Fig. 10